

Class19

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12/2/2021

Reading the downloaded file into R

```
mxl <- read.table("file.txt")  
head(mxl)
```

```
##      sample geno      exp  
## 1 HG00367  A/G 28.96038  
## 2 NA20768  A/G 20.24449  
## 3 HG00361  A/A 31.32628  
## 4 HG00135  A/A 34.11169  
## 5 NA18870  G/G 18.25141  
## 6 NA11993  A/A 32.89721
```

Q13

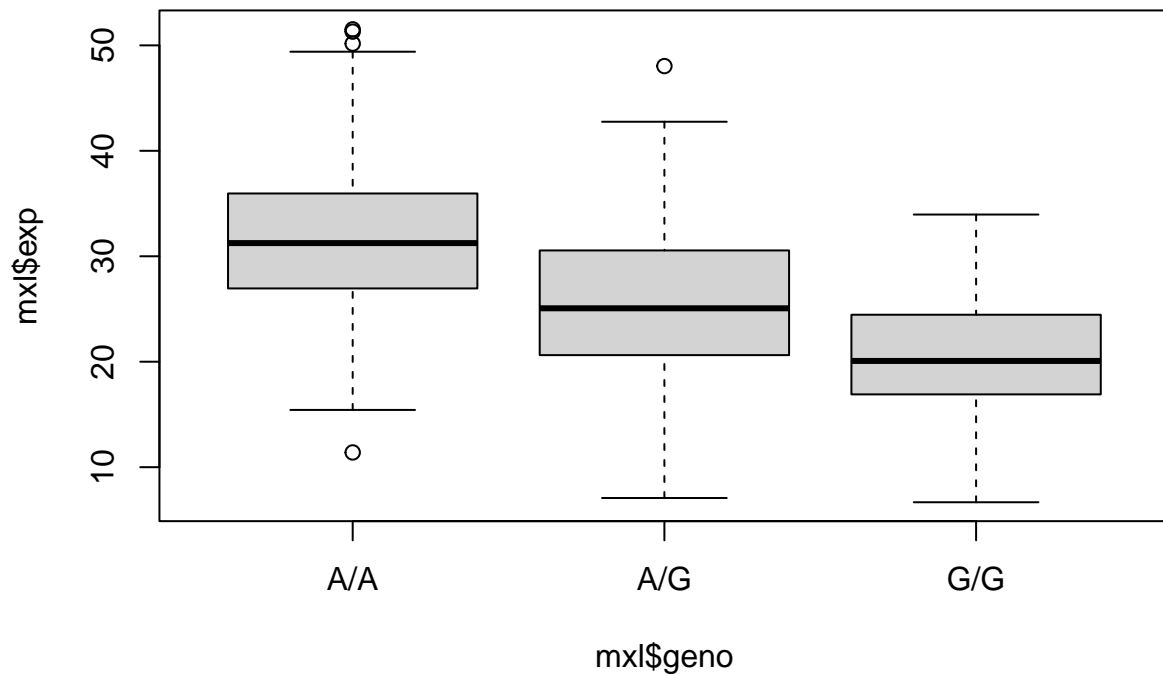
```
table(mx1$geno)
```

```
##  
## A/A A/G G/G  
## 108 233 121
```

```
table(mx1$geno)/nrow(mx1)*100
```

```
##  
##      A/A      A/G      G/G  
## 23.37662 50.43290 26.19048
```

```
graph <- boxplot(mx1$exp~mx1$geno, data=mx1)
```



Median for each genotype correspond to the black line in each box:

```
print(graph$stats)
```

```
##           [,1]      [,2]      [,3]
## [1,] 15.42908  7.07505  6.67482
## [2,] 26.95022 20.62572 16.90256
## [3,] 31.24847 25.06486 20.07363
## [4,] 35.95503 30.55183 24.45672
## [5,] 49.39612 42.75662 33.95602
```

Medians=

A/A: 31.24847 ; A/G: 25.06486 ; G/G: 20.07363

Q14

```
library(ggplot2)
```

```
ggplot(mx1) + aes(x=geno, y= exp, fill=geno) + geom_boxplot(notch=TRUE)
```

